

SEQUENCE LISTING

```
<110> Gressel, Jonathan
     Eyal, Yoram
     Fluhr, Robert
<120> RHAMNOSYL-TRANSFERASE GENE AND USES THEREOF
<130> 01/22289
<140> US 09/889,738
<141> 2000-01-20
<150>
      IL 128193
<151> 1999-01-20
<150> PCT/IL00/00038
<151> 2000-01-20
<160> 21
<170> PatentIn version 3.1
<210> 1
<211>
      8
<212>
      PRT
<213> Citrus X paradisi
<400> 1
Asn Tyr Phe Leu His Leu Thr Ala
<210>
      2
<211>
      3
<212>
      PRT
<213> Citrus X paradisi
<400> 2
Tyr Pro Phe
<210>
       3
<211>
      7
<212> PRT
<213> Citrus X paradisi
<400> 3
Ile Ala Ala Ile Leu Phe Leu
<210>
<211>
      8
<212>
      PRT
<213> Citrus X paradisi
<400> 4
```

Tyr Phe Pro Ser Leu Met Gly Asn

HECEIVED DEC 0 7 2001 TECH CENTER 1600/2900

```
<210> 5
<211> 8
<212> PRT
<213> Citrus X paradisi
<400> 5
Glu Lys Met Thr Ile Glu Glu Ala
<210> 6
<211> 4
<212> PRT
<213> Citrus X paradisi
<400> 6
Leu Phe Gln Pro
<210> 7
<211> 14
<212> PRT
<213> Citrus X paradisi
<400> 7
Val Val Asp Asn Gly Met Gly Met Val Val Pro Arg Asp Lys
                 5
<210> 8
<211> 20
<212> DNA
<213> Artificial sequence
<220>
<223> Synthetic oligonucleotide
<220>
<221> misc_feature
<222>
       (9)..(9)
<223> Modified base : Inosine
<220>
<221> misc_feature <222> (15)..(15)
<223> Modified base : Inosine
<400> 8
                                                                             20
gayaayggna tgggnatggt
<210> 9
<211> 7
<212> PRT
<213> Citrus X paradisi
<400> 9
```

```
Asp Asn Gly Met Gly Met Val
           5
<210> 10
<211> 23
<212> DNA
<213> Artificial sequence
<220>
<223> Synthetic oligonucleotide
<220>
<221> misc_feature
<222> (12)..(12)
<223> Modified base: Inosine
<400> 10
garaaratga cnathgarga rgc
                                                                       23
<210> 11
<211>
      23
<212> DNA
<213> Artificial sequence
<220>
<223> Synthetic oligonucleotide
<220>
<221> misc_feature
<222>
      (12)^{-}. (12)
<223> Modified base : Inosine
<220>
<221> misc_feature
<222>
      (18)..(18)
<223> Modified base : Inosine
<220>
<221> misc_feature
<222>
       (21)..(21)
<223> Modified base : Inosine
<400> 11
                                                                       23
aaytayttyc tncayctnac ngc
<210> 12
<211> 8
<212> PRT
<213> Citrus X paradisi
<400> 12
Asn Tyr Phe Leu His Leu Thr Ala
                5
```

<210> <211>

<210> 13

			4				
•	•						
•							
	<211>						
_	<212>						
	<213>	Artificial sequence					
	<220>						
	<223>	Synthetic oligonucleotide					
		1.2					
	<400>					33	
	gettee	ccag tcacgacgtt ttttttttt ttt				33	
	.0.4.0						i
	<210> <211>						
	<211>						
		Artificial sequence					
		•					
	<220>						
	<223>	Synthetic oligonucleotide					
	<400>	14		•			
	gttttc	ccag tcacgacg				18	
	<210>	15					
	<211>						
	<212>						
	<213>	Artificial sequence .					
	<220>						
		Synthetic oligonucleotide					
-							
	<400>					• •	
	catgcc	cata ccattgtc				18	
*							
	<210>						
	<211>						
	<212>						
	<213>	Artificial sequence					
	<220>					•	
		Synthetic oligonucleotide					
		·					
	<400>	16 ggta tgggcatg				18	
	yacaac	ggta tyggtaty			•	10	
	<210>	17					
	<211>						
	<212>						
	<213>	Artificial sequence					
	<220>						
	<223>	Synthetic oligonucleotide					
	<400>	17					
		ccac cgagccccaa ccac				24	
	Z210N	1.0					
	<210> <211>						
	<211>						
		Artificial sequence					
	<220>						

<223> Synthetic oligonucleotide							
<400> 18 catctagaat ggataccaag catcaag							
<210> 19 <211> 29 <212> DNA <213> Artificial sequence							
<220> <223> Synthetic oligonucleotide							
<400> 19 caggatcctt attcagattt cttgacaag	29						
<210> 20 <211> 1359 <212> DNA <213> Citrus X paradisi							
<400> 20 '							
atggatacca agcatcaaga taagccaagc attetcatgt taccatgget ageteatggg	60						
cacatagete cacacettga acttgecaag aagettteae agaaaaaett eeacatatat	120						
ttotgotota otoccaacaa totacaatoo ttoggoagaa atgttgaaaa aaacttotoa	180						
tottoaatao aactoataga actgoaactt cocaatacat toottgaact toottoacaa	240						
aatcagacca caaaaaacct teeteeccat ettatttata etetegtggg ageatttgaa	300						
gacgcaaaac ctgctttttg caacatcttg gagacgctta aaccaaccct tgttatgtat	360						
gatttgttcc aaccgatggc ggcggaggca gcttaccagt atgacatagc tgctattttg	420						
ttcttaccct tatctgcagt agcctgctct ttcttgctgc acaatatcgt aaatcccagc	480						
ctgaaatacc ctttctttga atctgattac caagatagag aaagcaagaa catcaattac	540						
ttcctgcatc ttactgccaa tggcacctta aacaaagaca ggttcttaaa agctttcgaa	600						
ctatcttgca aatttgtgtt catcaaaaca tcaagagaga ttgaatccaa gtacttggat	660						
tattttcctt ctttaatggg aaatgaaata attccagtag ggcctctaat ccaagaacct	720						
accttcaagg tagatgatac aaagatcatg gactggctga gccaaaaagga gcctcgttca	780						
gtcgtgtatg catcctttgg cagtgagtac tttccttcca cggatgaaat acatgacata	840						
gctattgggt tattgctcac cgaggttaat tttatatggg ctttcagatt acatcctgat	900						
gagaaaatga cgatagagga agcactgcct cagggctttg ctgaggagat tgaaaggaat	960						
aataagggaa tgatagtaca aggttgggtt ccgcaggcta aaattttaag gcatggaagc	1020						
·	1080						
atcggcggat ttttgagtca ttgtggttgg ggctcggtgg ttgaggggat ggttttcggg	1140						
gtaccaatca taggtgtgcc aatggcatat gagcagccaa gcaatgccaa ggtggtggtt							
gacaatggta tgggcatggt cgttccaaga gataagatca atcaaagact tggaggagag	1200						
gaggtggcga gggtcattaa acatgttgtg ctgcaagaag aagcgaagca aataagaaga	1260						

1320

1359

aaagctaatg aaattagtga gagtatgaag aagatagggg acgcacagat gagtgtggtg

gtggagaaac tgctgcagct tgtcaagaaa tctgaataa <210> 21 <211> 452 <212> PRT <213> Citrus X paradisi <400> 21 Met Asp Thr Lys His Gln Asp Lys Pro Ser Ile Leu Met Leu Pro Trp 10 Leu Ala His Gly His Ile Ala Pro His Leu Glu Leu Ala Lys Lys Leu Ser Gln Lys Asn Phe His Ile Tyr Phe Cys Ser Thr Pro Asn Asn Leu Gln Ser Phe Gly Arg Asn Val Glu Lys Asn Phe Ser Ser Ile Gln Leu Ile Glu Leu Gln Leu Pro Asn Thr Phe Pro Glu Leu Pro Ser Gln 70 75 Asn Gln Thr Thr Lys Asn Leu Pro Pro His Leu Ile Tyr Thr Leu Val 85 Gly Ala Phe Glu Asp Ala Lys Pro Ala Phe Cys Asn Ile Leu Glu Thr Leu Lys Pro Thr Leu Val Met Tyr Asp Leu Phe Gln Pro Met Ala Ala 115 120 Glu Ala Ala Tyr Gln Tyr Asp Ile Ala Ala Ile Leu Phe Leu Pro Leu Ser Ala Val Ala Cys Ser Phe Leu Leu His Asn Ile Val Asn Pro Ser 155 Leu Lys Tyr Pro Phe Phe Glu Ser Asp Tyr Gln Asp Arg Glu Ser Lys 170 Asn Ile Asn Tyr Phe Leu His Leu Thr Ala Asn Gly Thr Leu Asn Lys 185 180

Asp Arg Phe Leu Lys Ala Phe Glu Leu Ser Cys Lys Phe Val Phe Ile 195 200 205 Lys Thr Ser Arg Glu Ile Glu Ser Lys Tyr Leu Asp Tyr Phe Pro Ser 210 215 220

Leu Met Gly Asn Glu Ile Ile Pro Val Gly Pro Leu Ile Gln Glu Pro 225 235 240

Thr Phe Lys Val Asp Asp Thr Lys Ile Met Asp Trp Leu Ser Gln Lys 245 250 255

Glu Pro Arg Ser Val Val Tyr Ala Ser Phe Gly Ser Glu Tyr Phe Pro 260 265 270

Ser Thr Asp Glu Ile His Asp Ile Ala Ile Gly Leu Leu Thr Glu 275 280 285

Val Asn Phe Ile Trp Ala Phe Arg Leu His Pro Asp Glu Lys Met Thr 290 295 300

Ile Glu Glu Ala Leu Pro Gln Gly Phe Ala Glu Glu Ile Glu Arg Asn 305 310 315 320

Asn Lys Gly Met Ile Val Gln Gly Trp Val Pro Gln Ala Lys Ile Leu 325 330 335

Arg His Gly Ser Ile Gly Gly Phe Leu Ser His Cys Gly Trp Gly Ser 340 345 350

Val Val Glu Gly Met Val Phe Gly Val Pro Ile Ile Gly Val Pro Met 355 \$360\$

Ala Tyr Glu Gln Pro Ser Asn Ala Lys Val Val Val Asp Asn Gly Met 370 375 380

Gly Met Val Val Pro Arg Asp Lys Ile Asn Gln Arg Leu Gly Glu 385 390 395 400

Glu Val Ala Arg Val Ile Lys His Val Val Leu Gln Glu Glu Ala Lys $405 \hspace{1.5cm} 410 \hspace{1.5cm} 415$

Gln Ile Arg Arg Lys Ala Asn Glu Ile Ser Glu Ser Met Lys Lys Ile 420 425 430

Gly Asp Ala Gln Met Ser Val Val Val Glu Lys Leu Leu Gln Leu Val 435 440 445

Lys Lys Ser Glu 450